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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=5; day=7; hr=15; min=2; sec=57; ms=396;]

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Application No: 10584362 Version No: 2.0

Input Set:

Output Set:

Started: 2009-05-01 08:41:20.339
Finished: 2009-05-01 08:41:25.191
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 852 ms
Total Warnings: 30
Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 852 ms
Total Warnings: 30
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 402	Undefined organism found in <213> in SEQ ID (27)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)

SEQUENCE LISTING

<110> Bos, Martine Petronella
Poolman, Jan
Tefsen, Boris
Tommassen, Johannes Petrus Maria

<120> OUTER MEMBRANE VESICLES AND USES THEREOF

<130> VB60639

<140> 10584362
<141> 2006-06-23

<150> PCT/EP2004/014770
<151> 2004-12-21

<150> GB 0329827.0
<151> 2003-12-23

<150> GB 0416398.6
<151> 2004-07-22

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 802
<212> PRT
<213> Neisseria

<400> 1
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1 5 10 15
Cys Phe Gly Thr His Cys Ala Ala Ala Asp Ala Val Ala Ala Glu Glu
20 25 30
Thr Asp Asn Pro Thr Ala Gly Glu Ser Val Arg Ser Val Ser Glu Pro
35 40 45
Ile Gln Pro Thr Ser Leu Ser Leu Gly Ser Thr Cys Leu Phe Cys Ser
50 55 60
Asn Glu Ser Gly Ser Pro Glu Arg Thr Glu Ala Ala Val Gln Gly Ser
65 70 75 80
Gly Glu Ala Ser Ile Pro Glu Asp Tyr Thr Arg Ile Val Ala Asp Arg
85 90 95
Met Glu Gly Gln Ser Gln Val Gln Val Arg Ala Glu Gly Asn Val Val
100 105 110
Val Glu Arg Asn Arg Thr Thr Leu Asn Thr Asp Trp Ala Asp Tyr Asp
115 120 125
Gln Ser Gly Asp Thr Val Thr Ala Gly Asp Arg Phe Ala Leu Gln Gln
130 135 140
Asp Gly Thr Leu Ile Arg Gly Glu Thr Leu Thr Tyr Asn Leu Glu Gln
145 150 155 160

Gln Thr Gly Glu Ala His Asn Val Arg Met Glu Ile Glu Gln Gly Gly
165 170 175
Arg Arg Leu Gln Ser Val Ser Arg Thr Ala Glu Met Leu Gly Glu Gly
180 185 190
His Tyr Lys Leu Thr Glu Thr Gln Phe Asn Thr Cys Ser Ala Gly Asp
195 200 205
Ala Gly Trp Tyr Val Lys Ala Ala Ser Val Glu Ala Asp Arg Glu Lys
210 215 220
Gly Ile Gly Val Ala Lys His Ala Ala Phe Val Phe Gly Gly Val Pro
225 230 235 240
Ile Phe Tyr Thr Pro Trp Ala Asp Phe Pro Leu Asp Gly Asn Arg Lys
245 250 255
Ser Gly Leu Leu Val Pro Ser Leu Ser Ala Gly Ser Asp Gly Val Ser
260 265 270
Leu Ser Val Pro Tyr Tyr Phe Asn Leu Ala Pro Asn Leu Asp Ala Thr
275 280 285
Phe Ala Pro Ser Val Ile Gly Glu Arg Gly Ala Val Phe Asp Gly Gln
290 295 300
Val Arg Tyr Leu Arg Pro Asp Tyr Ala Gly Gln Ser Asp Leu Thr Trp
305 310 315 320
Leu Pro His Asp Lys Lys Ser Gly Arg Asn Asn Arg Tyr Gln Ala Lys
325 330 335
Trp Gln His Arg His Asp Ile Ser Asp Thr Leu Gln Ala Gly Val Asp
340 345 350
Phe Asn Gln Val Ser Asp Ser Gly Tyr Tyr Arg Asp Phe Tyr Gly Asn
355 360 365
Lys Glu Ile Ala Gly Asn Val Asn Leu Asn Arg Arg Val Trp Leu Asp
370 375 380
Tyr Gly Arg Ala Ala Gly Gly Ser Leu Asn Ala Gly Leu Ser Val
385 390 395 400
Leu Lys Tyr Gln Thr Leu Ala Asn Gln Ser Gly Tyr Lys Asp Lys Pro
405 410 415
Tyr Ala Leu Met Pro Arg Leu Ser Val Glu Trp Arg Lys Asn Thr Gly
420 425 430
Arg Ala Gln Ile Gly Val Ser Ala Gln Phe Thr Arg Phe Ser His Asp
435 440 445
Ser Arg Gln Asp Gly Ser Arg Leu Val Val Tyr Pro Asp Ile Lys Trp
450 455 460
Asp Phe Ser Asn Ser Trp Gly Tyr Val Arg Pro Lys Leu Gly Leu His
465 470 475 480
Ala Thr Tyr Tyr Ser Leu Asn Arg Phe Gly Ser Gln Glu Ala Arg Arg
485 490 495
Val Ser Arg Thr Leu Pro Ile Val Asn Ile Asp Ser Gly Ala Thr Phe
500 505 510
Glu Arg Asn Thr Arg Met Phe Gly Gly Glu Val Leu Gln Thr Leu Glu
515 520 525
Pro Arg Leu Phe Tyr Asn Tyr Ile Pro Ala Lys Ser Gln Asn Asp Leu
530 535 540
Pro Asn Phe Asp Ser Ser Glu Ser Ser Phe Gly Tyr Gly Gln Leu Phe
545 550 555 560
Arg Glu Asn Leu Tyr Tyr Gly Asn Asp Arg Ile Asn Thr Ala Asn Ser
565 570 575
Leu Ser Ala Ala Val Gln Ser Arg Ile Leu Asp Gly Ala Thr Gly Glu
580 585 590
Glu Arg Phe Arg Ala Gly Ile Gly Gln Lys Phe Tyr Phe Lys Asp Asp
595 600 605
Ala Val Met Leu Asp Gly Ser Val Gly Lys Lys Pro Arg Asn Arg Ser

610	615	620
Asp Trp Val Ala Phe Ala Ser Gly Ser Ile Gly Ser Arg Phe Ile Leu		
625	630	635
Asp Ser Ser Ile His Tyr Asn Gln Asn Asp Lys Arg Ala Glu Asn Tyr		640
645	650	655
Ala Val Gly Ala Ser Tyr Arg Pro Ala Gln Gly Lys Val Leu Asn Ala		
660	665	670
Arg Tyr Lys Tyr Gly Arg Asn Glu Lys Ile Tyr Leu Lys Ser Asp Gly		
675	680	685
Ser Tyr Phe Tyr Asp Lys Leu Ser Gln Leu Asp Leu Ser Ala Gln Trp		
690	695	700
Pro Leu Thr Arg Asn Leu Ser Ala Val Val Arg Tyr Asn Tyr Gly Phe		
705	710	715
Glu Ala Lys Lys Pro Ile Glu Val Leu Ala Gly Ala Glu Tyr Lys Ser		
725	730	735
Ser Cys Gly Cys Trp Gly Ala Gly Val Tyr Ala Gln Arg Tyr Val Thr		
740	745	750
Gly Glu Asn Thr Tyr Lys Asn Ala Val Phe Phe Ser Leu Gln Leu Lys		
755	760	765
Asp Leu Ser Ser Val Gly Arg Asn Pro Ala Asp Arg Met Asp Val Ala		
770	775	780
Val Pro Gly Tyr Ile Thr Ala His Ser Leu Ser Ala Gly Arg Asn Lys		
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Arg Pro		800

<210> 2
<211> 621
<212> PRT
<213> N. meningitidis

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20	25	30
Val Ala Ala Leu Ile Ala Ile Phe Gly Val Ala Ala Thr Glu Ser Tyr		
35	40	45
Leu Ala Ala Phe Ile Ala Pro Leu Ile Asn His Gly Phe Ser Ala Pro		
50	55	60
Ala Ala Pro Pro Glu Leu Ser Ala Ala Gly Ile Ile Ser Thr Leu		
65	70	75
Gln Asn Trp Arg Glu Gln Phe Thr Tyr Met Val Trp Gly Thr Glu Asn		
85	90	95
Lys Ile Trp Thr Val Pro Leu Phe Leu Ile Leu Val Val Ile Arg		
100	105	110
Gly Ile Cys Arg Phe Thr Ser Thr Tyr Leu Met Thr Trp Val Ser Val		
115	120	125
Met Thr Ile Ser Lys Ile Arg Lys Asp Met Phe Ala Lys Met Leu Thr		
130	135	140
Leu Ser Ser Arg Tyr His Gln Glu Thr Pro Ser Gly Thr Val Leu Met		
145	150	155
Asn Met Leu Asn Leu Thr Glu Gln Ser Val Ser Asn Ala Ser Asp Ile		
165	170	175
Phe Thr Val Leu Thr Arg Asp Thr Met Ile Val Thr Gly Leu Thr Ile		
180	185	190

Val Leu Leu Tyr Leu Asn Trp Gln Leu Ser Leu Ile Val Val Leu Met
 195 200 205
 Phe Pro Leu Leu Ser Leu Leu Ser Arg Tyr Tyr Arg Asp Arg Leu Lys
 210 215 220
 His Val Ile Ser Asp Ser Gln Lys Ser Ile Gly Thr Met Asn Asn Val
 225 230 235 240
 Ile Ala Glu Thr His Gln Gly His Arg Val Val Lys Leu Phe Asn Gly
 245 250 255
 Gln Ala Gln Ala Ala Asn Arg Phe Asp Ala Val Asn Arg Thr Ile Val
 260 265 270
 Arg Leu Ser Lys Lys Ile Thr Gln Ala Thr Ala Ala His Ser Pro Phe
 275 280 285
 Ser Glu Leu Ile Ala Ser Ile Ala Leu Ala Val Val Ile Phe Ile Ala
 290 295 300
 Leu Trp Gln Ser Gln Asn Gly Tyr Thr Thr Ile Gly Glu Phe Met Ala
 305 310 315 320
 Phe Ile Val Ala Met Leu Gln Met Tyr Ala Pro Ile Lys Ser Leu Ala
 325 330 335
 Asn Ile Ser Ile Pro Met Gln Thr Met Phe Leu Ala Ala Asp Gly Val
 340 345 350
 Cys Ala Phe Leu Asp Thr Pro Pro Glu Gln Asp Lys Gly Thr Leu Ala
 355 360 365
 Pro Gln Arg Val Glu Gly Arg Ile Ser Phe Arg Asn Val Asp Val Glu
 370 375 380
 Tyr Arg Ser Asp Gly Ile Lys Ala Leu Asp Asn Phe Asn Leu Asp Ile
 385 390 395 400
 Arg Gln Gly Glu Arg Val Ala Leu Val Gly Arg Ser Gly Ser Gly Lys
 405 410 415
 Ser Thr Val Val Asn Leu Leu Pro Arg Phe Val Glu Pro Ser Ala Gly
 420 425 430
 Asn Ile Cys Ile Asp Gly Ile Asp Ile Ala Asp Ile Lys Leu Asp Cys
 435 440 445
 Leu Arg Ala Gln Phe Ala Leu Val Ser Gln Asp Val Phe Leu Phe Asp
 450 455 460
 Asp Thr Leu Phe Glu Asn Val Arg Tyr Ser Arg Pro Asp Ala Gly Glu
 465 470 475 480
 Ala Glu Val Leu Phe Ala Leu Gln Thr Ala Asn Leu Gln Ser Leu Ile
 485 490 495
 Asp Ser Ser Pro Leu Gly Leu His Gln Pro Ile Gly Ser Asn Gly Ser
 500 505 510
 Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Ala Arg Ala Ile
 515 520 525
 Leu Lys Asp Ala Pro Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu
 530 535 540
 Asp Asn Glu Ser Glu Arg Leu Val Gln Gln Ala Leu Glu Arg Leu Met
 545 550 555 560
 Glu Asn Arg Thr Gly Ile Ile Val Ala His Arg Leu Thr Thr Ile Glu
 565 570 575
 Gly Ala Asp Arg Ile Ile Val Met Asp Asp Gly Lys Ile Ile Glu Gln
 580 585 590
 Gly Thr His Glu Gln Leu Met Ser Gln Asn Gly Tyr Tyr Thr Met Leu
 595 600 605
 Arg Asn Ile Ser Asn Lys Asp Ala Ala Val Arg Thr Ala
 610 615 620

<211> 1866
<212> DNA
<213> *N. meningitidis*

<400> 3

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ggcgttgcgc ccaccgaaag ctacccgtcc gccttcatcg cccccctgtat taaccacggc 180
tttccgcac ctgcgcgcac gcccggagctg tctgcgcgc cccggatcat ttccaccctg 240
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gtcccgctct tcctcatcat cctcgctc atccgtggca tctgcgcgtt taccagcacc 360
tatctgtatga cttgggtctc cgtgtatgacc atcagcaaaa tccgcaaaaga tatgtttgcc 420
aaaatgtcga cccttcctc ccgctaccat cagggaaacgc cgtccggcac cgtactgtatg 480
aatatgtcga acctgaccga acagtggc agcaacgcca ggcacatctt caccgtcctc 540
acgcgcgaca cgatgtatcg taccggcctg accatcgatcc tgctttacct caactggcag 600
ctcagcccta tcgtcgctt gatgttcccc ctgctctccc tgctctcgcc ctactaccgc 660
gaccgtctga aacacgtcat ttccgactcg caaaaaaagca taggcacgt gaacaacgt 720
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gcaacggcgg cacattcccc gttcagcgaa ctgatcgctt cgatcgccct cggcgtcgcc 900
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cgctcgccca ttggccggcgc cattttggaaa gacgcqccga tattattatt ggacgaaagcc 1620
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atcatcgatcg tggacgacgg caaaatcatc gaacaaggca cacacgaaca actgtatgtcc 1800
caaaacggtt actacacgtat gttacgcaat atctcaaaca aagatgcccgc cgtccggacg 1860
gcataa 1866

1866

<210> 4

<211> 623

<212> PRT

<213> B. parapertussis

<400> 4

Met Leu Ala Trp Arg Pro Gly Arg Pro Asp Gly Cys Gln Ala Ala Gly

1 5 10 15

Gly Arg Arg Tyr Asn Pro Gly His Asp Cys Ile Lys Ala Ser Val Ser

20 25 30

Ser Ala Ala Arg Asn Ala Pro Ala Gly Ser Gl

35 40 45

Ala Glu Leu Trp Lys Arg Val Tyr Ser Arg Val Gly Ser Tyr

50 55 60

Gly Leu Val Leu Ala Val Leu Leu Met Ala Gly Ala Ala Ala Thr Gln

Pro Thr Leu Ala Val Ile Met Lys Pro Leu Leu Asp Asp Gly Phe Ser

100	105	110
Leu Ile Leu Leu Arg Gly Ile Cys Asn Phe Phe Ser Asp Tyr	Leu	
115	120	125
Ala Trp Val Ala Asn Asn Val Leu Arg Gly Ile Arg Gly Glu	Met	Phe
130	135	140
Glu Arg Leu Leu Gly Leu Pro Asp Ala Asp Phe Lys Arg Gly	Asp	Thr
145	150	155
Gly Arg Leu Leu Asn Arg Phe Thr Ile Asp Ala Gly Asn Val	Thr	Gly
165	170	175
Tyr Ala Thr Asp Val Ile Thr Val Leu Val Arg Glu Thr	Leu	Val Val
180	185	190
Ile Ala Leu Ile Gly Val Leu Leu Tyr Met Ser Trp Ala Leu	Thr	Leu
195	200	205
Ile Ile Leu Val Met Leu Pro Val Ser Val Gly Ile Ala Arg	Ala	Phe
210	215	220
Thr Arg Arg Leu Arg Arg Ile Asn Arg Glu Thr Val Asn Met	Asn	Ala
225	230	235
Glu Leu Thr Arg Val Val Ser Glu Gly Ile Asp Gly Gln Arg	Val	Ile
245	250	255
Lys Leu Phe Asp Gly Tyr Asp Ala Glu Arg Arg Arg Phe Asp	Phe	Val
260	265	270
Asn Ser Arg Leu Arg Arg Phe Ala Met Arg Ser Ala Thr	Ala	Asp Ala
275	280	285
Ala Leu Thr Pro Leu Thr Gln Val Cys Ile Ser Val Ala Val	Gly	Ala
290	295	300
Val Ile Ala Val Ala Leu Ser Gln Ala Asn Ser Gly Ala	Leu	Thr Val
305	310	315
Gly Ser Phe Ala Ser Phe Met Ala Ala Leu Ala Gln Ile Phe	Asp	Pro
325	330	335
Ile Lys Arg Leu Thr Asn Leu Ala Gly Lys Met Gln Lys Met	Leu	Val
340	345	350
Ala Ala Glu Ser Val Phe Thr Leu Val Asp Gln Thr Pro	Glu	Ala Asp
355	360	365
Ala Gly Thr Arg Ala Leu Pro Glu Pro Val Arg Gly Lys Val	Glu	Phe
370	375	380
Arg Ala Val Ser His Arg Phe Pro Asp Ala Asp Arg Asp Thr	V	